

RAW SEQUENCE LISTING

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Application Serial Number: 1015231277
Source: PCT
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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/523,277

DATE: 02/15/2005

TIME: 15:32:46

Input Set : A:\SAMSF342.txt

Output Set: N:\CRF4\02152005\J523277.raw

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3 <110> APPLICANT: SOUTH ALABAMA MEDICAL SCIENCES FOUNDATION
5 <120> TITLE OF INVENTION: CANCER VACCINES CONTAINING EPITOPES OF ONCOFETAL
6   ANTIGEN
8 <130> FILE REFERENCE: SAMSF 3.4-002
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/523,277
C--> 11 <141> CURRENT FILING DATE: 2005-02-01
13 <150> PRIOR APPLICATION NUMBER: 60/400,851
14 <151> PRIOR FILING DATE: 2002-08-02
16 <160> NUMBER OF SEQ ID NOS: 82
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1067
22 <212> TYPE: DNA
23 <213> ORGANISM: Mus musculus
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (86)..(970)
29 <400> SEQUENCE: 1
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32 cgtaacttaa agggaaactt acaca atg tcc gga gcc ctt gac gtc ctg cag 112
33                               Met Ser Gly Ala Leu Asp Val Leu Gln
34                               1           5
36 atg aag gag gag gat gtc ctc aaa ttc ctt gct gcg gga acc cac tta 160
37 Met Lys Glu Glu Asp Val Leu Lys Phe Leu Ala Ala Gly Thr His Leu
38 10           15           20           25
40 ggt ggc acc aac ctt gac ttt cag atg gag cag tac atc tac aaa agg 208
41 Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln Tyr Ile Tyr Lys Arg
42           30           35           40
44 aaa agt gac ggt atc tac atc ata aac ctg aag agg acc tgg gag aag 256
45 Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys Arg Thr Trp Glu Lys
46           45           50           55
48 ctg ttg ctc gca gct cga gct att gtt gcc atc gag aat cct gct gac 304
49 Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile Glu Asn Pro Ala Asp
50           60           65           70
52 gtc agc gtc atc tcc tcc agg aac act ggc cag cga gct gtg ctg aag 352
53 Val Ser Val Ile Ser Ser Arg Asn Thr Gly Gln Arg Ala Val Leu Lys
54           75           80           85
56 ttt gct gct gcc aca gga gcc act ccg atc gct ggc cgc ttc aca cct 400
57 Phe Ala Ala Ala Thr Gly Ala Thr Pro Ile Ala Gly Arg Phe Thr Pro
58 90           95           100           105
60 ggg acc ttc act aac cag atc caa gca gcc ttc agg gag cca cgg ctt 448
61 Gly Thr Phe Thr Asn Gln Ile Gln Ala Ala Phe Arg Glu Pro Arg Leu
62           110           115           120

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64 cta gtg gtg acc gat ccc agg gct gac cat cag cca ctc aca gag gcc 496
65 Leu Val Val Thr Asp Pro Arg Ala Asp His Gln Pro Leu Thr Glu Ala
66      125      130      135
68 tct tat gtc aac ctg ccc acc att gct ctg tgt aac aca gat tct ccc 544
69 Ser Tyr Val Asn Leu Pro Thr Ile Ala Leu Cys Asn Thr Asp Ser Pro
70      140      145      150
72 ctg cgc tat gtg gac att gcc atc cca tgc aac aac aag gga gct cac 592
73 Leu Arg Tyr Val Asp Ile Ala Ile Pro Cys Asn Asn Lys Gly Ala His
74      155      160      165
76 tca gtg ggt ctg atg tgg tgg atg ctg gcc agg gaa gta ctc cgc atg 640
77 Ser Val Gly Leu Met Trp Trp Met Leu Ala Arg Glu Val Leu Arg Met
78 170      175      180      185
80 cga ggt act atc tcc cgt gag cac ccc tgg gag gtc atg cct gat ctt 688
81 Arg Gly Thr Ile Ser Arg Glu His Pro Trp Glu Val Met Pro Asp Leu
82      190      195      200
84 tac ttc tac aga gac cca gag gag att gag aag gag gag cag gct gct 736
85 Tyr Phe Tyr Arg Asp Pro Glu Glu Ile Glu Lys Glu Glu Gln Ala Ala
86      205      210      215
88 gct gag aag gct gtg acc aag gag gaa ttc cag ggt gaa tgg acc gca 784
89 Ala Glu Lys Ala Val Thr Lys Glu Glu Phe Gln Gly Glu Trp Thr Ala
90      220      225      230
92 cca gct cct gag ttc act gct gct cag cct gag gtg gcc gac tgg tct 832
93 Pro Ala Pro Glu Phe Thr Ala Ala Gln Pro Glu Val Ala Asp Trp Ser
94      235      240      245
96 gag ggt gtg cag gtt ccc tct gtg ccc atc cag cag ttc ccc acg gaa 880
97 Glu Gly Val Gln Val Pro Ser Val Pro Ile Gln Gln Phe Pro Thr Glu
98 250      255      260      265
100 gac tgg agt gca cag cca gcc act gag gat tgg tca gca gct ccc aca 928
101 Asp Trp Ser Ala Gln Pro Ala Thr Glu Asp Trp Ser Ala Ala Pro Thr
102      270      275      280
104 gcg cag gcc act gag tgg gtt gga gcc acc act gag tgg tcc 970
105 Ala Gln Ala Thr Glu Trp Val Gly Ala Thr Thr Glu Trp Ser
106      285      290      295
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115 <212> TYPE: PRT
116 <213> ORGANISM: Mus musculus
118 <400> SEQUENCE: 2
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122 Lys Phe Leu Ala Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe
123 20 25 30
125 Gln Met Glu Gln Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile
126 35 40 45
128 Ile Asn Leu Lys Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala
129 50 55 60
131 Ile Val Ala Ile Glu Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg

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132 65          70          75          80
134 Asn Thr Gly Gln Arg Ala Val Leu Lys Phe Ala Ala Thr Gly Ala
135          85          90          95
137 Thr Pro Ile Ala Gly Arg Phe Thr Pro Gly Thr Phe Thr Asn Gln Ile
138          100          105          110
140 Gln Ala Ala Phe Arg Glu Pro Arg Leu Leu Val Val Thr Asp Pro Arg
141          115          120          125
143 Ala Asp His Gln Pro Leu Thr Glu Ala Ser Tyr Val Asn Leu Pro Thr
144          130          135          140
146 Ile Ala Leu Cys Asn Thr Asp Ser Pro Leu Arg Tyr Val Asp Ile Ala
147 145          150          155          160
149 Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp Trp
150          165          170          175
152 Met Leu Ala Arg Glu Val Leu Arg Met Arg Gly Thr Ile Ser Arg Glu
153          180          185          190
155 His Pro Trp Glu Val Met Pro Asp Leu Tyr Phe Tyr Arg Asp Pro Glu
156          195          200          205
158 Glu Ile Glu Lys Glu Glu Gln Ala Ala Ala Glu Lys Ala Val Thr Lys
159          210          215          220
161 Glu Glu Phe Gln Gly Glu Trp Thr Ala Pro Ala Pro Glu Phe Thr Ala
162 225          230          235          240
164 Ala Gln Pro Glu Val Ala Asp Trp Ser Glu Gly Val Gln Val Pro Ser
165          245          250          255
167 Val Pro Ile Gln Gln Phe Pro Thr Glu Asp Trp Ser Ala Gln Pro Ala
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171          275          280          285
173 Gly Ala Thr Thr Glu Trp Ser
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178 <211> LENGTH: 1067
179 <212> TYPE: DNA
180 <213> ORGANISM: Mus musculus
182 <220> FEATURE:
183 <221> NAME/KEY: CDS
184 <222> LOCATION: (86)..(970)
186 <400> SEQUENCE: 3
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189 cgtaacttaa agggaaactt acaca atg tcc gga gcc ctt gac gtc ctg cag 112
190          Met Ser Gly Ala Leu Asp Val Leu Gln
191          1          5
193 atg aag gag gag gat gtc ctc aaa ctc ctt gct gcg gga acc cac tta 160
194 Met Lys Glu Glu Asp Val Leu Lys Leu Leu Ala Ala Gly Thr His Leu
195 10          15          20          25
197 ggt ggc acc aac ctt gac ttt cag atg gag cag tac atc tac aaa agg 208
198 Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln Tyr Ile Tyr Lys Arg
199          30          35          40
201 aaa agt gac ggt atc tac atc ata aac ctg aag agg acc tgg gag aag 256
202 Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys Arg Thr Trp Glu Lys

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203          45          50          55
205 ctg ttg ctc gca gct cga gct att gtt gcc atc gag aat cct gct gac 304
206 Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile Glu Asn Pro Ala Asp
207          60          65          70
209 gtc agc gtc atc tcc tcc agg aac act ggc cag cga gct gtg ctg aag 352
210 Val Ser Val Ile Ser Ser Arg Asn Thr Gly Gln Arg Ala Val Leu Lys
211          75          80          85
213 ttt gct gct gcc aca gga gcc act ccg atc gct ggc cgc ttc aca cct 400
214 Phe Ala Ala Ala Thr Gly Ala Thr Pro Ile Ala Gly Arg Phe Thr Pro
215 90          95          100          105
217 ggg acc ttc act aac cag atc caa gca gcc ttc agg gag cca cgg ctt 448
218 Gly Thr Phe Thr Asn Gln Ile Gln Ala Ala Phe Arg Glu Pro Arg Leu
219          110          115          120
221 cta gtg gtg acc gat ccc agg gct gac cat cag cca ctc aca gag gcc 496
222 Leu Val Val Thr Asp Pro Arg Ala Asp His Gln Pro Leu Thr Glu Ala
223          125          130          135
225 tct tat gtc aac ctg ccc acc att gct ctg tgt aac aca gat tct ccc 544
226 Ser Tyr Val Asn Leu Pro Thr Ile Ala Leu Cys Asn Thr Asp Ser Pro
227          140          145          150
229 ctg gcg tat gtg gac att gcc atc cca tgc aac aac aag gga gct cac 592
230 Leu Ala Tyr Val Asp Ile Ala Ile Pro Cys Asn Asn Lys Gly Ala His
231          155          160          165
233 tca gtg ggt ctg atg tgg tgg atg ctg gcc agg gaa gta ctc cgc atg 640
234 Ser Val Gly Leu Met Trp Trp Met Leu Ala Arg Glu Val Leu Arg Met
235 170          175          180          185
237 cga ggt act atc tcc cgt gag cac ccc tgg gag gtc atg cct gat ctt 688
238 Arg Gly Thr Ile Ser Arg Glu His Pro Trp Glu Val Met Pro Asp Leu
239          190          195          200
241 tac ttc tac aga gac cca gag gag att gag aag gag gag cag gct gct 736
242 Tyr Phe Tyr Arg Asp Pro Glu Glu Ile Glu Lys Glu Glu Gln Ala Ala
243          205          210          215
245 gct gag aag gct gtg acc aag gag gaa ttc cag ggt gaa tgg acc gca 784
246 Ala Glu Lys Ala Val Thr Lys Glu Glu Phe Gln Gly Glu Trp Thr Ala
247          220          225          230
249 cca gct cct gag ttc act gct gct cag cct gag gtg gcc gac tgg tct 832
250 Pro Ala Pro Glu Phe Thr Ala Ala Gln Pro Glu Val Ala Asp Trp Ser
251          235          240          245
253 gag ggt gtg cag gtt ccc tct gtg ccc atc cag cag ttc ccc acg gaa 880
254 Glu Gly Val Gln Val Pro Ser Val Pro Ile Gln Gln Phe Pro Thr Glu
255 250          255          260          265
257 gac tgg agt gca cag cca gcc act gag gat tgg tca gca gct ccc aca 928
258 Asp Trp Ser Ala Gln Pro Ala Thr Glu Asp Trp Ser Ala Ala Pro Thr
259          270          275          280
261 gcg cag gcc act gag tgg gtt gga gcc acc act gag tgg tcc 970
262 Ala Gln Ala Thr Glu Trp Val Gly Ala Thr Thr Glu Trp Ser
263          285          290          295
265 tgagctgctg tgcaggtgcc tgagcaaagg gaaaaaagat ggaaggaaaa taaagttgct 1030
267 aaaagctgaa aaaaaaaaaa aaaaaaaggg cggccgc 1067
270 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING

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Input Set : A:\SAMSF342.txt

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271 <211> LENGTH: 295

272 <212> TYPE: PRT

273 <213> ORGANISM: Mus Musculus

275 <400> SEQUENCE: 4

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279 Lys Leu Leu Ala Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe
280           20           25           30
282 Gln Met Glu Gln Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile
283           35           40           45
285 Ile Asn Leu Lys Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala
286           50           55           60
288 Ile Val Ala Ile Glu Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg
289   65           70           75           80
291 Asn Thr Gly Gln Arg Ala Val Leu Lys Phe Ala Ala Ala Thr Gly Ala
292           85           90           95
294 Thr Pro Ile Ala Gly Arg Phe Thr Pro Gly Thr Phe Thr Asn Gln Ile
295           100          105          110
297 Gln Ala Ala Phe Arg Glu Pro Arg Leu Leu Val Val Thr Asp Pro Arg
298           115          120          125
300 Ala Asp His Gln Pro Leu Thr Glu Ala Ser Tyr Val Asn Leu Pro Thr
301           130          135          140
303 Ile Ala Leu Cys Asn Thr Asp Ser Pro Leu Ala Tyr Val Asp Ile Ala
304 145           150          155          160
306 Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp Trp
307           165          170          175
309 Met Leu Ala Arg Glu Val Leu Arg Met Arg Gly Thr Ile Ser Arg Glu
310           180          185          190
312 His Pro Trp Glu Val Met Pro Asp Leu Tyr Phe Tyr Arg Asp Pro Glu
313           195          200          205
315 Glu Ile Glu Lys Glu Glu Gln Ala Ala Ala Glu Lys Ala Val Thr Lys
316           210          215          220
318 Glu Glu Phe Gln Gly Glu Trp Thr Ala Pro Ala Pro Glu Phe Thr Ala
319 225          230          235          240
321 Ala Gln Pro Glu Val Ala Asp Trp Ser Glu Gly Val Gln Val Pro Ser
322           245          250          255
324 Val Pro Ile Gln Phe Pro Thr Glu Asp Trp Ser Ala Gln Pro Ala
325           260          265          270
327 Thr Glu Asp Trp Ser Ala Ala Pro Thr Ala Gln Ala Thr Glu Trp Val
328           275          280          285
330 Gly Ala Thr Thr Glu Trp Ser
331           290          295

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334 <210> SEQ ID NO: 5

335 <211> LENGTH: 295

336 <212> TYPE: PRT

337 <213> ORGANISM: Homo sapiens

339 <400> SEQUENCE: 5

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VERIFICATION SUMMARYPATENT APPLICATION: **US/10/523,277**

DATE: 02/15/2005

TIME: 15:32:47

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date